

ABSTRACT OF THE DISCLOSURE

MLVA methods for strain discrimination among *Mycobacterium tuberculosis strains* are disclosed. Nine VNTR loci have been identified from genomic sequences of *Mycobacterium tuberculosis* strains and primer pairs suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. This sub-typing scheme is useful for the epidemiological study of *Mycobacterium tuberculosis* and may be applied to the local detection of the pathological causative agent of tuberculosis.